

OM protein - protein search, using sw model

Run on: May 19, 2004, 16:52:51 ; Search time 63.75 Seconds  
(without alignments)  
66.482 Million cell updates/sec

Title: US-10-034-974-7  
Perfect score: 104

Sequence: 1 WKACPGEDWLFQWGS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	15	5 AAE26735	Aae26735 Fibrin bi
2	73	70.2	15	5 AAE26758	Aae26758 Fibrin bi
3	70	67.3	15	5 AAE26762	Aae26762 Fibrin bi
4	66	63.5	15	5 AAE26733	Aae26733 Fibrin bi
5	66	63.5	19	5 AAE26744	Aae26744 Slow diss
6	66	63.5	19	5 AAE26745	Aae26745 Slow diss
7	66	63.5	19	5 AAE26743	Aae26743 Slow diss
8	63	60.6	9	5 AAE26753	Aae26753 Fibrin bi
9	63	60.6	15	5 AAE26732	Aae26732 Fibrin bi

10	60	57.7	15	5 AAE26731	Aae26731 Fibrin bi
11	57	54.8	15	5 AAE26764	Aae26764 Fibrin bi
12	56	53.8	15	5 AAE26765	Aae26765 Fibrin bi
13	56	53.8	15	5 AAE26766	Aae26766 Fibrin bi
14	54.5	52.4	51	4 AAU61462	AAU61462 Propionib
15	54.5	52.4	51	6 ABM57981	ABM57981 Propionib
16	53.5	51.4	4347	4 ABM59051	ABM59051 Drosophil
17	51	49.0	9	5 AAE26777	Aae26777 Fibrin bi
18	51	49.0	9	5 AAE26778	Aae26778 Fibrin bi
19	51	49.0	15	5 AAE26761	Aae26761 Fibrin bi
20	51	49.0	33	2 AAU40294	AAU40294 Human con
21	51	49.0	255	5 ABP45903	ABP45903 Human Bly
22	50.5	48.6	34	2 AAU06189	AAU06189 Anti-angi
23	50	48.1	9	5 AAE26780	Aae26780 Fibrin bi
24	50	48.1	15	5 AAE26734	Aae26734 Fibrin bi
25	50	48.1	19	5 AAE26746	Aae26746 Slow diss
26	50	48.1	19	5 AAE26748	Aae26748 Slow diss
27	50	48.1	19	5 AAE26747	Aae26747 Slow diss
28	48	46.2	9	5 AAE26774	Aae26774 Fibrin bi
29	48	46.2	270	4 ABG30149	ABG30149 Novel hum
30	47	45.2	93	4 ABG24468	ABG24468 Novel hum
31	46.5	44.7	85	5 ABP43519	ABP43519 Human sec
32	46	44.2	98	4 ABM50783	ABM50783 Human sec
33	46	44.2	98	6 ABO45040	ABO45040 Novel hum
34	46	44.2	98	7 ABO26520	ABO26520 Protein a
35	46	44.2	339	6 ABU23786	ABU23786 Protein e
36	46	44.2	347	3 AAG13457	Aag13457 Arabidops
37	46	44.2	347	3 AAG52967	Aag52967 Arabidops
38	46	44.2	365	3 AAG52966	Aag52966 Arabidops
39	46	44.2	365	3 AAG13456	Aag13456 Arabidops
40	46	44.2	423	3 AAG52965	Aag52965 Arabidops
41	46	44.2	423	3 AAG13455	Aag13455 Arabidops
42	46	44.2	1695	4 AAB83975	Aab83975 Amino aci
43	45.5	43.8	169	2 AAY60559	Aay60558 Human nor
44	45.5	43.8	289	4 AAB93469	Aab93469 Human pro
45	45.5	43.8	580	4 AAU16207	AAU16207 Human nov

#### ALIGNMENTS

RESULT 1  
AAE26735  
ID AAE26735 standard; peptide; 15 AA.  
XX  
XX  
AC AAE26735;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Fibrin binding peptide #6.  
XX

Fibrin binding peptide; thrombosis; pulmonary embolism; atherosclerosis;  
KW myocardial infarct; ischaemia; imaging; rheumatoid arthritis; vasotrophic;  
KW anaemia; hypoxia; tumour; diabetic retinopathy; autoimmune disorder;  
KW inflammatory disorder; angiogenesis; stroke; cerebroprotective.  
XX  
OS Unidentified.

XX PN WO20025544-A2.  
XX PD 18-JUL-2002.  
XX PF 21-DEC-2001; 2001WO-US049534.  
XX PR 23-DEC-2000; 2000US-00747403.  
XX PA (DYAX-) DVAX CORP.  
XX PI Wescott CR, Beltzer JP, Sato AK;  
XX DR WPI; 2002-666875/71.  
XX PT Novel synthetic fibrin-binding moiety, useful for detecting, imaging or  
XX localizing fibrin-containing clots by magnetic resonance imaging,  
XX radioimaging and for treating diseases involving thrombus formation e.g.  
XX stroke.  
XX PS Claim 10; Page 57; 69pp; English.  
XX

XX The invention relates to a synthetic fibrin binding group having affinity  
CC for fibrin. The invention is useful for detecting fibrin in a mammalian  
CC subject which involves (a) detectably labelling the binding group; (b)  
CC administering to the subject the labelled polypeptide, and (c) detecting  
CC the labelled polypeptide in the subject. The invention is useful for  
CC treating a disease involving thrombus formation eg. deep-vein thrombosis,  
CC pulmonary embolism, cardiogenic thrombosis, atherosclerosis, myocardial  
CC infarct, reperfusion ischaemia or stroke. The binding moieties are useful  
CC for detection, imaging and localisation of fibrin-containing clots by  
CC magnetic resonance imaging, radioimaging and other imaging methods and  
CC are also useful in the diagnosis and treatment of coronary conditions  
CC where fibrin plays a role. The fibrin binding moieties are useful for  
CC detecting and diagnosing numerous pathologies in which fibrin plays  
CC a role eg. peritoneal adhesions which often occur after surgery or  
CC inflammatory and neoplastic processes and are comprised of a fibrin  
CC network, fibroblasts, macrophages and new blood vessels; rheumatoid  
CC arthritis, lupus or septic arthritis which often have bits of fibrin  
CC containing tissues called rice bodies in the synovial fluid of their  
CC joints; thrombocytopenic purpura, a type of anaemia in which deposits in  
CC arterioles causes turbulent blood flow resulting in stress and  
CC destruction of red blood cells. The fibrin specific agents can also be  
CC used to detect hypoxia or ischaemia of heart, kidney, liver, lung, brain  
CC or other organs, as well as the detection of tumours, diabetic  
CC retinopathy, early or high-risk atherosclerosis and other autoimmune and  
CC inflammatory disorders. Fibrin specific agents also could provide both  
CC direct or surrogate markers of disease models in which hypoxia and  
CC angiogenesis are expected to play a role. The invention is also useful  
CC for screening molecular libraries. The present sequence is a fibrin  
CC binding peptide  
XX

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 104; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred.No. 2.6e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: May 19, 2004, 17:07:54 ; Search time 51.875 Seconds  
(without alignments)  
80.461 Million cell updates/sec

Title: US-10-034-974-7

Perfect score: 104

Sequence: 1 WKACPGEDWLFQWGS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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RESULT 1  
US-10-034-974-7  
; Sequence 7, Application US/10034974  
; Publication No. US20030143158A1  
; GENERAL INFORMATION:  
; APPLICANT: DYAX CORP.

#### ALIGNMENTS

1	104	100.0	15	14	US-10-034-974-7	Sequence 7, Appli
2	73	70.2	15	14	US-10-034-974-30	Sequence 30, Appl
3	70	67.3	15	14	US-10-034-974-34	Sequence 34, Appl
4	66	63.5	15	14	US-10-034-974-5	Sequence 5, Appli
5	66	63.5	19	14	US-10-034-974-15	Sequence 15, Appl
6	66	63.5	19	14	US-10-034-974-16	Sequence 16, Appl
7	66	63.5	19	14	US-10-034-974-17	Sequence 17, Appl
8	63	60.6	9	14	US-10-034-974-25	Sequence 25, Appl
9	63	60.6	15	14	US-10-034-974-4	Sequence 4, Appli
10	60	57.7	15	14	US-10-034-974-3	Sequence 3, Appli
11	57	54.8	15	14	US-10-034-974-36	Sequence 36, Appl
12	56	53.8	15	14	US-10-034-974-37	Sequence 37, Appl
13	56	53.8	15	14	US-10-034-974-38	Sequence 38, Appl
14	51	49.0	9	14	US-10-034-974-49	Sequence 49, Appl
15	51	49.0	9	14	US-10-034-974-50	Sequence 50, Appl
16	51	49.0	15	14	US-10-034-974-33	Sequence 33, Appl
17	51	49.0	25	10	US-09-880-748-1914	Sequence 1914, Ap
18	51	49.0	25	12	US-10-293-416-1914	Sequence 15, Appl
19	50.5	48.6	34	13	US-10-036-869-15	Sequence 15, Appl
20	50	48.1	9	14	US-10-034-974-52	Sequence 52, Appl
21	50	48.1	15	14	US-10-034-974-6	Sequence 6, Appli
22	50	48.1	15	14	US-10-034-974-18	Sequence 18, Appl
23	50	48.1	19	14	US-10-034-974-19	Sequence 19, Appl
24	50	48.1	19	14	US-10-034-974-20	Sequence 20, Appl
25	49	47.1	379	14	US-10-029-386-32938	Sequence 32938, A
26	48	46.2	9	14	US-10-034-974-46	Sequence 46, Appl
27	46	44.2	65	12	US-10-434-599-194290	Sequence 194290,
28	46	44.2	98	10	US-09-933-767-736	Sequence 736, App
29	46	44.2	98	12	US-10-004-860-736	Sequence 736, App
30	46	44.2	98	14	US-10-023-282-736	Sequence 736, App
31	46	44.2	339	12	US-10-282-122A-51710	Sequence 51710, A
32	45.5	43.8	580	9	US-09-764-864-1160	Sequence 1160, A
33	45.5	43.8	1047	15	US-10-094-749-2629	Sequence 2629, Ap
34	45	43.3	26	14	US-10-058-053A-303	Sequence 303, App
35	45	43.3	37	14	US-10-058-053A-287	Sequence 287, App
36	45	43.3	37	14	US-10-058-053A-288	Sequence 288, App
37	45	43.3	37	14	US-10-058-053A-289	Sequence 289, App
38	45	43.3	44	12	US-10-632-983-104	Sequence 104, App
39	45	43.3	80	14	US-10-058-053A-110	Sequence 110, App
40	45	43.3	96	12	US-10-632-983-103	Sequence 103, App
41	45	43.3	101	12	US-10-424-599-144611	Sequence 144611,
42	45	43.3	109	14	US-10-058-053A-143	Sequence 143, App
43	45	43.3	110	14	US-10-058-053A-167	Sequence 167, App
44	45	43.3	110	14	US-10-058-053A-173	Sequence 173, App
45	45	43.3	494	12	US-10-425-114-65620	Sequence 65620, A

; APPLICANT: Beltzer, James P.  
 ; APPLICANT: Wescott, Charles R.  
 ; APPLICANT: Sato, Aaron K.  
 ; TITLE OF INVENTION: FIBRIN BINDING MOETIES USEFUL AS IMAGING AGENTS  
 ; FILE REFERENCE: DIX-024.1 PCT; DIX-024.1 US  
 ; CURRENT APPLICATION NUMBER: US/10/034,974  
 ; PRIOR FILING DATE: 2001-12-21  
 ; PRIOR APPLICATION NUMBER: US 09/747,403  
 ; NUMBER OF SEQ ID NOS: 56  
 ; SOFTWARE: Patent version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: fibrin binding polypeptide  
 US-10-034-974-7  
  
 Query Match 100.0%; Score 104; DB 14; Length 15;  
 Best Local Similarity 100.0%; Pred.No. 3.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 WKACPGEDWLCWGS 15  
 |||||  
 Db 1 WKACPGEDWLCWGS 15  
  
 Search completed: May 19, 2004, 17:17:35  
 Job time : 58.875 secs

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 OM protein - protein search, using sw model  
  
 Run on: May 19, 2004, 16:59:56 ; Search time 16.875 Seconds  
 (without alignments)  
 85.504 Million cell updates/sec

Title: US-10-034-974-7  
 Perfect score: 104  
 Sequence: 1 WKACPGEDWLCWGS 15  
  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
  
 Searched: 283366 seqs, 96191526 residues  
  
 Total number of hits satisfying chosen parameters: 283366  
  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries  
  
 Database : PIR\_78:  
 1: pir1:  
 2: pir2:  
 3: pir3:  
 4: pir4:

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	48.1	215	2 JCS114	glutathione transf
2	47	45.2	624	2 S74222	alpha-galactosidas
3	46	44.2	339	2 F97190	phenylalanyl-tRNA
4	46	44.2	423	2 G85255	CDP-diacylglycerol
5	46	44.2	423	2 T04915	CDP-diacylglycerol
6	45.5	43.8	1633	2 JCS056	polydromo 1 - chic
7	45	43.3	119	2 T46478	hypothetical prote
8	45	43.3	242	2 G83281	hypothetical prote
9	45	43.3	499	2 S28306	hypothetical prote
10	45	43.3	532	2 E69343	2-oxoacid-ferredox
11	45	43.3	579	2 D88551	protein T2305.5 (i
12	45	43.3	615	2 T43330	catecholamine tran
13	44	42.3	217	2 S54138	probable coat prot

14 44 42.3 259 2 F36899  
15 44 42.3 259 2 S35136  
16 44 42.3 277 2 F66777  
17 44 42.3 458 2 A56055  
18 44 42.3 651 2 D86977  
19 43 41.3 292 2 G88071  
20 43 41.3 297 2 A82832  
21 43 41.3 297 2 F97609  
22 43 41.3 3036 2 T18995  
23 42.5 40.9 148 2 A86079  
24 42.5 40.9 148 2 B91232  
25 42.5 40.9 148 2 D86849  
26 42 40.4 195 2 D96341  
27 42 40.4 236 2 B70488  
28 42 40.4 346 2 T35363  
29 42 40.4 437 2 G97298  
30 42 40.4 558 2 E91170  
31 42 40.4 558 2 E86016  
32 42 40.4 590 2 A56335  
33 42 40.4 820 2 E95980  
34 42 40.4 822 2 D87325  
35 42 40.4 922 2 T23573  
36 42 40.4 943 2 S59317  
37 41.5 39.9 203 2 A53234  
38 41.5 39.9 889 2 S51455  
39 41 39.4 250 2 B22454  
40 41 39.4 292 2 A83779  
41 41 39.4 353 1 F2VF01  
42 41 39.4 429 2 T21113  
43 41 39.4 438 2 T04800  
44 41 39.4 521 2 T18896  
45 41 39.4 538 2 H70379

leuD 3'-region hyp  
hypothetical prote  
ABC transporter AT  
CAP59 protein - Or  
Probable primosoma  
protein ZK1240.5 (l  
aminoglycoside pho  
hypothetical prote  
hypothetical prote  
PTS system, fructo  
PTS system, fructo  
frvA protein - Esc  
hypothetical prote  
cytochrome-c oxida  
D-alanine-D-alanin  
hypothetical prote  
hypothetical prote  
probable enzyme 24  
gadd34 protein - l  
probable nitrite r  
nitrite reductase  
hypothetical prote  
DIP2 protein - yea  
superoxide dismuta  
hypothetical prote  
probable thioredox  
hypothetical prote  
photosystem II pro  
hypothetical prote  
CDP-diacylglycerol  
glypican 1 precurs  
hypothetical prote

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OK protein - protein search, using sw model

Run on: May 19, 2004, 16:56:57 ; Search time 12.5 Seconds  
(without alignments)  
62.484 Million cell updates/sec

Title: US-10-034-974-7  
Perfect score: 104  
Sequence: 1 WRACPFEDWLCWGS 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Query Match %	Length	DB ID		
1	46	44.2	339	1	SYFA_CLOAB	O97qk9 Clostridium
2	46	44.2	1199	1	Y173_HUMAN	Q14879 homo sapien
3	45	43.3	615	1	NTDO_CAEEL	Q03614 caenorhabdi
4	44	42.3	259	1	YMEB_LACLA	Q02151 lactococcus
5	44	42.3	651	1	PRIA_MYCLE	Q9ccq3 mycobacteri
6	42.5	40.9	148	1	PTVA_ECOLI	P32155 escherichia
7	42	40.4	237	1	TRPF_PICPA	O13504 pichia past
8	42	40.4	321	1	FCL_HUMAN	O13630 homo sapien
9	42	40.4	346	1	VANL_STRCO	Q9xak7 streptomyce
10	42	40.4	943	1	DIP2_YEAST	Q12220 saccharomyc
11	41.5	39.9	889	1	RSC2_YEAST	Q06488 saccharomyc
12	41	39.4	250	1	TDXH_AERPE	Q9y910 aeropyrum p
13	41	39.4	254	1	PRMA_THETH	Q84bq9 thermus the
14	41	39.4	365	1	FXH1_HUMAN	O75593 homo sapien
15	41	39.4	413	1	WDR4_MOUSE	Q9ep82 mus musculu
16	41	39.4	441	1	EMO1_HUMAN	Q96a84 homo sapien
17	41	39.4	444	1	EMO1_MOUSE	Q91vr5 mus musculu

Search completed: May 19, 2004, 17:08:25  
Job time : 17.875 secs

18 41 39.4 465 1 GFR2\_CHICK  
19 41 39.4 687 1 C1CL\_RAT  
20 41 39.4 725 1 NC42\_MOUSE  
21 40 38.5 273 1 SCAB\_RANCA  
22 40 38.5 421 1 CDS1\_ARATH  
23 40 38.5 521 1 VENV\_DHV11  
24 40 38.5 522 1 AOF\_ONCMY  
25 40 38.5 621 1 GLGB\_RHOMR  
26 40 38.5 655 1 PRIA\_MYCTU  
27 40 38.5 725 1 GUNG\_CLOCE  
28 40 38.5 866 1 F1BA\_HUMAN  
29 39.5 38.0 531 1 P111\_MOUSE  
30 39.5 38.0 2352 1 MORC\_SCHPO  
31 39.5 38.0 2616 1 NDL\_DROME  
32 39 37.5 62 1 VKIL\_BPP22  
33 39 37.5 106 1 YB91\_YEAST  
34 39 37.5 201 1 YMW3\_YEAST  
35 39 37.5 206 1 EBRP\_HUMAN  
36 39 37.5 398 1 GSP1\_KLEPN  
37 39 37.5 410 1 TX28\_HUMAN  
38 39 37.5 424 1 CDS1\_SOLTU  
39 39 37.5 445 1 ENV\_MLVER  
40 39 37.5 452 1 E2BG\_HUMAN  
41 39 37.5 513 1 AMY3\_SCHPO  
42 39 37.5 521 1 YF92\_MYCPN  
43 39 37.5 536 1 THIP\_ECOLI  
44 39 37.5 603 1 FOXB\_LACPL  
45 39 37.5 646 1 SCE2\_XENLA

OM protein - protein search, using sw model  
Run on: May 19, 2004, 16:58:07 ; Search time 45.625 Seconds  
(without alignments)  
103.732 Million cell updates/sec  
Title: US-10-034-974-7  
Perfect score: 104  
Sequence: 1 WACPGDWLFCWGS 15  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SPTREMBL\_25:  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriac:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
Description					

1	53.5	51.4	1952	5	Q95SN5	Q95sn5 drosophila
2	53.5	51.4	4547	5	Q9W343	Q9w343 drosophila
3	52	50.0	365	12	Q91TQ6	Q91tq6 tupaia herp
4	50	48.1	215	10	Q42706	Q42706 coccomyxa s
5	50	48.1	217	12	Q8V323	Q8v323 citrus vari
6	50	48.1	217	12	Q8V325	Q8v325 citrus vari
7	49	47.1	467	10	Q941V5	Q941v5 oryza sativ
8	48	46.2	558	11	Q8CA33	Q8ca33 mus musculu
9	47.5	45.7	144	2	Q8RQV1	Q8rqv1 bacillus gl
10	47.5	45.7	661	16	Q7UR25	Q7ur25 rhodopirell
11	47	45.2	157	11	Q8BLH8	Q8blh8 mus musculu
12	47	45.2	185	11	Q8BKJ6	Q8bkj6 mus musculu
13	47	45.2	624	3	Q92451	Q92451 trichoderma
14	46	44.2	302	16	Q7U6X7	Q7u6x7 synchococc
15	46	44.2	315	16	Q9KYU8	Q9kyu8 streptomyce
16	46	44.2	423	10	Q49639	Q49639 arabidopsis
17	46	44.2	889	16	Q82V65	Q82v65 nitrosomona
18	46	44.2	1199	4	Q8W29	Q8w29 homo sapien
19	45.5	43.8	289	4	Q9NUX9	Q9nux9 homo sapien
20	45.5	43.8	503	10	Q9M3B9	Q9m3b9 chlamydomon
21	45.5	43.8	551	5	Q9GRT8	Q9grt8 leishmania
22	45.5	43.8	605	5	Q9GYD0	Q9gyd0 leishmania
23	45.5	43.8	1047	4	Q96MS2	Q96ms2 homo sapien
24	45.5	43.8	1582	4	Q9H2T3	Q9ht23 homo sapien
25	45.5	43.8	1602	4	Q9H2T5	Q9ht25 homo sapien
26	45.5	43.8	1633	13	Q90941	Q90941 gallus gall
27	45.5	43.8	1634	4	Q9H314	Q9h314 homo sapien
28	45.5	43.8	1689	4	Q86U86	Q86u86 homo sapien
29	45	43.3	119	4	Q9NSV2	Q9nsv2 homo sapien
30	45	43.3	120	11	Q8C4A2	Q8c4a2 mus musculu
31	45	43.3	144	4	Q9HBQ8	Q9hbq8 homo sapien
32	45	43.3	217	12	Q86106	Q86106 citrus leaf
33	45	43.3	242	16	Q9H2T8	Q9ht28 pseudomonas
34	45	43.3	315	16	Q8F9F7	Q8f9f7 leptospira
35	45	43.3	384	10	Q7X920	Q7x920 oryza sativ
36	45	43.3	393	16	Q82TM7	Q82tm7 nitrosomona
37	45	43.3	428	10	Q9FSJ6	Q9fsj6 oryza sativ
38	45	43.3	532	17	Q29509	Q29509 archaeoglob
39	45	43.3	1053	16	Q9RKY93	Q9rk93 streptomyce
40	44.5	42.8	434	5	Q7YZS7	Q7yzs7 ciona intes
41	44	42.3	212	12	Q99HQ7	Q99hq7 tulare appl
42	44	42.3	217	12	Q8V322	Q8v322 citrus vari
43	44	42.3	217	12	Q8V321	Q8v321 citrus vari
44	44	42.3	217	12	Q8V324	Q8v324 citrus vari
45	44	42.3	217	12	Q8V326	Q8v326 citrus vari

Search completed: May 19, 2004, 17:07:46  
Job time : 47.625 secs

OM protein - protein search, using sw model

Run on: May 19, 2004, 16:52:51 ; Search time 38.25 Seconds  
(without alignments)  
66.482 Million cell updates/sec

Title: US-10-034-974-25  
Perfect score: 63  
Sequence: 1 CPGEWLF 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues  
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003s:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	9	5 AAE26753	Aae26753 Fibrin bi
2	63	100.0	15	5 AAE26735	Aae26735 Fibrin bi
3	51	81.0	9	5 AAE26777	Aae26777 Fibrin bi
4	51	81.0	9	5 AAE26778	Aae26778 Fibrin bi
5	51	81.0	15	5 AAE26762	Aae26762 Fibrin bi
6	51	81.0	15	5 AAE26761	Aae26761 Fibrin bi
7	50	79.4	9	5 AAE26780	Aae26780 Fibrin bi
8	50	79.4	15	5 AAE26764	Aae26764 Fibrin bi
9	48	76.2	9	5 AAE26774	Aae26774 Fibrin bi

10	48	76.2	15	5 AAE26758	Aae26758 Fibrin bi
11	44	69.8	9	5 AAE26751	Aae26751 Fibrin bi
12	44	69.8	15	5 AAE26733	Aae26733 Fibrin bi
13	44	69.8	19	5 AAE26744	Aae26744 Slow diss
14	44	69.8	19	5 AAE26745	Aae26745 Slow diss
15	44	69.8	19	5 AAE26743	Aae26743 Slow diss
16	42	66.7	9	5 AAE26750	Aae26750 Fibrin bi
17	42	66.7	15	5 AAE26732	Aae26732 Fibrin bi
18	42	66.7	147	4 AAU28117	AAU28117 Novel hum
19	42	66.7	314	3 AAY81361	AAY81361 Human GDP
20	42	66.7	321	2 AAY28286	AAY28286 Amino aci
21	42	66.7	321	3 AAY54116	AAY54116 A GDP-4-k
22	42	66.7	321	6 AAG007263	AAG007263 Human p53
23	42	66.7	435	4 AAU28305	AAU28305 Novel hum
24	42	66.7	595	5 ABP69754	ABP69754 Human pol
25	42	66.7	595	6 ABR82247	ABR82247 Human nuc
26	42	66.7	1165	4 ABB00133	ABB00133 Novel hum
27	41	65.1	1222	4 ABB11946	ABB11946 Human pre
28	41	65.1	1222	4 AAV79508	AAV79508 Human pro
29	40.5	64.3	4547	4 ABB59051	ABB59051 Drosophila
30	40	63.5	9	5 AAE26752	Aae26752 Fibrin bi
31	40	63.5	15	5 AAE26734	Aae26734 Fibrin bi
32	40	63.5	19	5 AAE26746	Aae26746 Slow diss
33	40	63.5	19	5 AAE26748	Aae26748 Slow diss
34	40	63.5	19	5 AAE26747	Aae26747 Slow diss
35	40	63.5	21	5 ABA47152	ABA47152 Human Bly
36	40	63.5	121	4 AAO11054	AAO11054 Human pol
37	40	63.5	255	5 ABP45903	ABP45903 Human Bly
38	40	63.5	316	4 ABG22448	ABG22448 Novel hum
39	40	63.5	943	6 ABR53214	ABR53214 Protein s
40	40	63.5	1658	4 ABG06029	ABG06029 Novel hum
41	39	61.9	60	4 AAU39512	AAU39512 Propionib
42	39	61.9	60	6 ABM36031	ABM36031 Propionib
43	39	61.9	166	3 ABA43631	ABA43631 Human can
44	39	61.9	194	5 ABB80581	ABB80581 Human seg
45	39	61.9	200	4 ABG04658	ABG04658 Novel hum

ALIGNMENTS

RESULT 1  
AAE26753  
ID AAE26753 standard; peptide; 9 AA.  
XX  
AC AAE26753;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Fibrin binding loop #5.  
XX

KW Fibrin binding peptide; thrombosis; pulmonary embolism; atherosclerosis;  
KW myocardial infarct; ischaemia; imaging; rheumatoid arthritis; vasotropic;  
KW anaemia; hypoxia; tumour; diabetic retinopathy; autoimmune disorder;  
KW inflammatory disorder; angiogenesis; stroke; cerebroprotective.  
XX  
OS Unidentified.



XX WO200255544-A2.  
 PN 18-JUL-2002.  
 XX 21-DEC-2001; 2001WO-US049534.  
 PD 23-DEC-2000; 2000US-00747403.  
 XX (DYAX-) DYAX CORP.  
 XX Wescott CR, Beltzer JP, Sato AK;  
 PI WPI; 2002-666875/71.  
 XX Novel synthetic fibrin-binding moiety, useful for detecting, imaging or  
 XX localizing fibrin-containing clots by magnetic resonance imaging,  
 XX radioimaging and for treating diseases involving thrombus formation e.g.  
 XX stroke.  
 XX Claim 4; Page 55; 89pp; English.  
 XX The invention relates to a synthetic fibrin binding group having affinity  
 XX for fibrin. The invention is useful for detecting fibrin in a mammalian  
 CC subject which involves (a) detectably labelling the binding group; (b)  
 CC administering to the subject the labelled polypeptide, and (c) detecting  
 CC the labelled polypeptide in the subject. The invention is useful for  
 CC treating a disease involving thrombus formation eg. deep-vein thrombosis,  
 CC pulmonary embolism, cardiogenic thrombosis, atherosclerosis, myocardial  
 CC infarct, reperfusion ischaemia or stroke. The binding moieties are useful  
 CC for detection, imaging and localisation of fibrin-containing clots by  
 CC magnetic resonance imaging, radioimaging and other imaging methods and  
 CC are also useful in the diagnosis and treatment of coronary conditions  
 CC where fibrin plays a role. The fibrin binding moieties are useful for  
 CC detecting and diagnosing numerous pathophysiological in which fibrin plays  
 CC a role eg. peritoneal adhesions which often occur after surgery or  
 CC inflammatory and neoplastic processes and are comprised of a fibrin  
 CC network, fibroblasts, macrophages and new blood vessels; rheumatoid  
 CC arthritis, lupus or septic arthritis which often have bits of fibrin  
 CC containing tissues called rice bodies in the synovial fluid of their  
 CC joints; thrombocytopenic purpura, a type of anaemia in which deposits in  
 CC arterioles causes turbulent blood flow resulting in stress and  
 CC destruction of red blood cells. The fibrin specific agents can also be  
 CC used to detect hypoxia or ischaemia of heart, kidney, liver, lung, brain  
 CC or other organs, as well as the detection of tumours, diabetic  
 CC retinopathy, early or high-risk atherosclerosis and other autoimmune and  
 CC inflammatory disorders. Fibrin specific agents also could provide both  
 CC direct or surrogate markers of disease models in which hypoxia and  
 CC angiogenesis are expected to play a role. The invention is also useful  
 CC for screening molecular libraries. The present sequence is a fibrin  
 CC binding loop  
 XX Sequence 9 AA;  
 XX Query Match 100.0%; Score 63; DB 5; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPGEDWLFC 9  
 XX | | | | | | | |  
 Db 1 CPGEDWLFC 9  
 RESULT 2  
 AAE26735  
 ID AAE26735 standard; peptide; 15 AA.  
 XX AAE26735;  
 AC AAE26735;  
 XX 13-DEC-2002 (first entry)  
 DT Fibrin binding peptide #6.  
 XX Fibrin binding peptide; thrombosis; pulmonary embolism; atherosclerosis;  
 XX myocardial infarct; ischaemia; imaging; rheumatoid arthritis; vasotropic;  
 KW anaemia; hypoxia; tumour; diabetic retinopathy; autoimmune disorder;  
 KW inflammatory disorder; angiogenesis; stroke; cerebroprotective.  
 XX Unidentified.  
 OS WO200255544-A2.  
 XX 18-JUL-2002.  
 PD 21-DEC-2001; 2001WO-US049534.  
 PF 23-DEC-2000; 2000US-00747403.  
 PR (DYAX-) DYAX CORP.  
 XX Wescott CR, Beltzer JP, Sato AK;  
 PI WPI; 2002-666875/71.  
 XX Novel synthetic fibrin-binding moiety, useful for detecting, imaging or  
 XX localizing fibrin-containing clots by magnetic resonance imaging,  
 XX radioimaging and for treating diseases involving thrombus formation e.g.  
 XX stroke.  
 XX Claim 10; Page 57; 89pp; English.  
 PS The invention relates to a synthetic fibrin binding group having affinity  
 CC for fibrin. The invention is useful for detecting fibrin in a mammalian  
 CC subject which involves (a) detectably labelling the binding group; (b)  
 CC administering to the subject the labelled polypeptide, and (c) detecting  
 CC the labelled polypeptide in the subject. The invention is useful for  
 CC treating a disease involving thrombus formation eg. deep-vein thrombosis,  
 CC pulmonary embolism, cardiogenic thrombosis, atherosclerosis, myocardial  
 CC infarct, reperfusion ischaemia or stroke. The binding moieties are useful  
 CC for detection, imaging and localisation of fibrin-containing clots by  
 CC magnetic resonance imaging, radioimaging and other imaging methods and  
 CC are also useful in the diagnosis and treatment of coronary conditions  
 CC where fibrin plays a role. The fibrin binding moieties are useful for  
 CC detecting and diagnosing numerous pathophysiological in which fibrin plays

CC a role eg. peritoneal adhesions which often occur after surgery or  
CC inflammatory and neoplastic processes and are comprised of a fibrin  
CC network, fibroblasts, macrophages and new blood vessels; rheumatoid  
CC arthritis, lupus or septic arthritis which often have bits of fibrin  
CC containing tissues called rice bodies in the synovial fluid of their  
CC joints; thrombocytopenic purpura, a type of anaemia in which deposits in  
CC arterioles causes turbulent blood flow resulting in stress and  
CC destruction of red blood cells. The fibrin specific agents can also be  
CC used to detect hypoxia or ischaemia of heart, kidney, liver, lung, brain  
CC or other organs, as well as the detection of tumours, diabetic  
CC retinopathy, early or high-risk atherosclerosis and other autoimmune and  
CC inflammatory disorders. Fibrin specific agents also could provide both  
CC direct or surrogate markers of disease models in which hypoxia and  
CC angiogenesis are expected to play a role. The invention is also useful  
CC for screening molecular libraries. The present sequence is a fibrin  
CC binding peptide  
XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 63; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CPGEDWLCF 9  
Db 4 CPGEDWLCF 12  
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Search completed: May 19, 2004, 17:05:47  
Job time : 39.25 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 19, 2004, 17:07:54 ; Search time 31.125 Seconds  
(without alignments)  
80.461 Million cell updates/sec

Title: US-10-034-974-25  
Perfect score: 63  
Sequence: 1 CPGEDWLCF 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query	DB	ID	Description
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Sequence 7, Appl  
Sequence 49, Appl  
Sequence 50, Appl  
Sequence 33, Appl  
Sequence 34, Appl  
Sequence 52, Appl  
Sequence 36, Appl  
Sequence 46, Appl  
Sequence 30, Appl  
Sequence 23, Appl  
Sequence 5, Appl  
Sequence 15, Appl  
Sequence 16, Appl  
Sequence 17, Appl  
Sequence 22, Appl  
Sequence 4, Appl  
Sequence 286, Appl  
Sequence 286, Appl  
Sequence 6, Appl  
Sequence 662, Appl  
Sequence 2316, Appl  
Sequence 24, Appl  
Sequence 6, Appl  
Sequence 18, Appl  
Sequence 19, Appl  
Sequence 20, Appl  
Sequence 3163, Appl  
Sequence 201051, Appl  
Sequence 216530, Appl  
Sequence 237281, Appl  
Sequence 1914, Appl  
Sequence 158986, Appl  
Sequence 1076, Appl  
Sequence 8487, Appl  
Sequence 209980, Appl  
Sequence 2223, Appl  
Sequence 21, Appl  
Sequence 53, Appl  
Sequence 3, Appl  
Sequence 37, Appl  
Sequence 265394, Appl

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8 50 79.4 15 14 US-10-034-974-36  
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17 42 66.7 15 14 US-10-034-974-4  
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19 42 66.7 147 15 US-10-291-172-286  
20 42 66.7 321 9 US-09-318-271-6  
21 42 66.7 455 12 US-10-221-278-662  
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37 39 61.9 166 9 US-09-925-301-1076  
38 39 61.9 592 15 US-10-369-493-8487  
39 38.5 61.1 77 12 US-10-424-599-209980  
40 38.5 61.1 513 15 US-10-369-493-2223  
41 38 60.3 9 14 US-10-034-974-21  
42 38 60.3 9 14 US-10-034-974-53  
43 38 60.3 15 14 US-10-034-974-3  
44 38 60.3 15 14 US-10-034-974-37  
45 38 60.3 106 12 US-10-424-599-265394

APPLICANT: Beltzer, James P.  
APPLICANT: Wescott, Charles R.  
APPLICANT: Sato, Aaron K.  
TITLE OF INVENTION: FIBRIN BINDING MOIETIES USEFUL AS IMAGING AGENTS  
FILE REFERENCE: DYX-024.1 PCT; DYX-024.1 US  
CURRENT APPLICATION NUMBER: US/10/034,974  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: US 09/747,403  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 25  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fibrin binding loop  
US-10-034-974-25

Query Match 100.0% Score 63; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPGEWLF 9  
Db 1 CPGEWLF 9  
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RESULT 2  
US-10-034-974-7  
Sequence 7, Application US/10034974  
Publication No. US20030143158A1  
GENERAL INFORMATION:  
APPLICANT: DYAX CORP.  
APPLICANT: Beltzer, James P.  
APPLICANT: Wescott, Charles R.  
APPLICANT: Sato, Aaron K.  
TITLE OF INVENTION: FIBRIN BINDING MOIETIES USEFUL AS IMAGING AGENTS  
FILE REFERENCE: DYX-024.1 PCT; DYX-024.1 US  
CURRENT APPLICATION NUMBER: US/10/034,974  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: US 09/747,403  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fibrin binding polypeptide  
US-10-034-974-7

Query Match 100.0% Score 63; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0039;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

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US-10-034-974-25  
Sequence 25, Application US/10034974  
Publication No. US20030143158A1  
GENERAL INFORMATION:  
APPLICANT: DYAX CORP.

QY 1 CPGEDWLFC 9  
DB 4 CPGEDWLFC 12

Search completed: May 19, 2004, 17:17:36  
Job time : 32.125 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 19, 2004, 16:59:56 ; Search time 10.125 Seconds  
(without alignments)  
85.504 Million cell updates/sec

Title: US-10-034-974-25  
Perfect score: 63  
Sequence: 1 CPGEDWLFC 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query			DB ID	Description
		Match	Length	%		
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3	40	63.5	943	2	S59317	DIP2 protein - yea
4	39	61.9	743	2	C56655	transducin-like en
5	38.5	61.1	513	2	T38770	alpha-amylase a pr
6	38	60.3	271	1	S12516	hypothetical prote
7	38	60.3	279	2	AH2408	permease protein o
8	38	60.3	1035	2	T16588	hypothetical prote
9	37	58.7	137	2	E86251	protein F25C20.8 f
10	37	58.7	144	2	G82092	conserved hypothet
11	37	58.7	262	2	A75009	probable aryl phos
12	37	58.7	388	2	E86239	protein F20524.2 f
13	37	58.7	423	2	G85255	CDP-diacylglycerol

14 37 58.7 423 2 T04915 CDP-diacylglycerol  
15 37 58.7 598 2 S51456 probable membrane  
16 37 58.7 599 2 S67094 probable membrane  
17 37 58.7 626 2 I49100 mscd6 precursor -  
18 37 58.7 1574 2 T13934 MEG56 protein - ra  
19 37 58.7 2241 2 T16064 hypothetical prote  
20 36.5 57.9 104 2 T49766 hypothetical prote  
21 36.5 57.9 346 2 T1263 xylene monooxygena  
22 36 57.1 99 2 B53116 Ig epsilon chain C  
23 36 57.1 126 2 C53116 Ig epsilon chain C  
24 36 57.1 182 2 D65005 hypothetical prote  
25 36 57.1 182 2 B91030 probable transport  
26 36 57.1 182 2 C65874 probable heme bind  
27 36 57.1 201 2 S52833 cytosine-specific  
28 36 57.1 331 2 T13145 hypothetical prote  
29 36 57.1 388 2 T15075 hypothetical prote  
30 36 57.1 467 2 T19233 sulfite reductase  
31 36 57.1 599 1 H65057 sulfite reductase  
32 36 57.1 599 2 C91081 sulfite reductase  
33 36 57.1 599 2 D85926 fibrinogen alpha c  
34 36 57.1 644 1 FG8UA 3-methyl-2-oxobuta  
35 36 57.1 678 2 G71526 3-methyl-2-oxobuta  
36 36 57.1 678 2 C81683 chloride channel p  
37 36 57.1 805 2 S13410 voltage-gated chor  
38 36 57.1 810 2 S19725 chloride channel p  
39 36 57.1 822 2 S68210 fibrinogen alpha c  
40 36 57.1 866 2 D4234 nitrate reductase  
41 36 57.1 889 2 T02240 chloride channel p  
42 36 57.1 907 2 S23399 chloride channel p  
43 36 57.1 988 2 S37078 chloride channel p  
44 36 57.1 994 2 S19595 chloride channel p  
45 36 57.1 1030 2 I35987 lantibiotic subtil

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OM protein - protein search, using sw model

Run on: May 19, 2004, 16:56:57 ; Search time 7.5 Seconds  
(without alignments)  
62.484 Million cell updates/sec

Title: US-10-034-974-25  
Perfect score: 63  
Sequence: 1 CPGEDMFC 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	42	66.7	321 1	FCL_HUMAN
2	40	63.5	943 1	DIP2_YEAST
3	39	61.9	743 1	TLE2_HUMAN
4	39	61.9	767 1	TLE2_MOUSE
5	38.5	61.1	513 1	AMY3_SCHPO
6	38	60.3	321 1	FCL_CRIGR
7	38	60.3	321 1	FCL_MOUSE
8	38	60.3	463 1	ENGA_BIFLO
9	37	58.7	598 1	THI7_YEAST
10	37	58.7	599 1	THI7_YEAST
11	37	58.7	665 1	CD6_MOUSE
12	36	57.1	182 1	YFOM_ECOLI
13	36	57.1	201 1	YMW3_YEAST
14	36	57.1	598 1	CYSJ_ECOLI
15	36	57.1	805 1	CICH_TORMA
16	36	57.1	809 1	CICH_TORCA
17	36	57.1	866 1	F15A_HUMAN
				Q13630 homo sapien
				Q12220 saccharomyc
				Q04725 homo sapien
				Q9wb22 mus musculu
				Q14154 schizosacch
				Q8kx22 cricetulus
				P23591 mus musculu
				Q8g6a8 bifidobacte
				Q05998 saccharomyc
				Q08579 saccharomyc
				Q61003 mus musculu
				P76398 escherichia
				Q04772 saccharomyc
				P38038 escherichia
				P21564 torpedo mar
				P35522 torpedo cal
				P02671 homo sapien

Search completed: May 19, 2004, 17:06:27  
Job time : 12.125 secs

18 36 57.1 869 1 NIA3\_MAIZE  
19 36 57.1 898 1 CLC2\_HUMAN  
20 36 57.1 898 1 CLC2\_RABIT  
21 36 57.1 902 1 CLC2\_CAVPO  
22 36 57.1 907 1 CLC2\_RAT  
23 36 57.1 908 1 CLC2\_MOUSE  
24 36 57.1 988 1 CLC1\_HUMAN  
25 36 57.1 994 1 CLC1\_MOUSE  
26 36 57.1 994 1 CLC1\_RAT  
27 36 57.1 1030 1 SPAB\_BACSU  
28 35 55.6 233 1 YJ75\_YEAST  
29 35 55.6 382 1 NIEV\_RHOCA  
30 35 55.6 670 1 NUSM\_WHEAT  
31 35 55.6 672 1 Y959\_MYCTU  
32 35 55.6 820 1 SYFB\_DEIRA  
33 35 55.6 882 1 HSI1\_HUMAN  
34 35 55.6 882 1 HSI1\_RAT  
35 35 55.6 925 1 NRP2\_RAT  
36 35 55.6 931 1 NRP2\_HUMAN  
37 35 55.6 931 1 NRP2\_MOUSE  
38 35 55.6 2261 1 NRPL\_MUNPM  
39 34.5 54.8 704 1 MEFB\_MOUSE  
40 34.5 54.8 704 1 MEFB\_RAT  
41 34.5 54.8 1010 1 AIA3\_CHICK  
42 34.5 54.8 1013 1 AIA3\_HUMAN  
43 34.5 54.8 1013 1 AIA3\_RAT  
44 34.5 54.8 1021 1 AIA1\_CHICK  
45 34.5 54.8 1022 1 AIA1\_ANGAN

P49102 zea mays (m  
P51788 homo sapien  
P51789 oryctolagus  
Q9WU45 cavia porce  
P35525 rattus norv  
Q9R0A1 mus musculu  
P35523 homo sapien  
Q64347 mus musculu  
P35524 rattus norv  
P39774 bacillus su  
P39541 saccharomyc  
Q07179 rhodobacter  
Q37680 triticum ae  
P71351 mycobacteri  
Q9RRX5 deinococcus  
P52848 homo sapien  
Q02353 rattus norv  
Q35276 rattus norv  
O60462 homo sapien  
O35375 mus musculu  
P30929 mumps virus  
Q61847 mus musculu  
P28826 rattus norv  
P24798 gallus gall  
P13637 homo sapien  
P06687 rattus norv  
P09572 gallus gall  
Q92030 anguilla an

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OM protein - protein search, using sw model

Run on: May 19, 2004, 16:58:07 ; Search time 27.375 Seconds  
(without alignments)  
103.732 Million cell updates/sec

Title: US-10-034-974-25  
Perfect score: 63  
Sequence: 1 CPGEWMLFC 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25: +  
1: sp\_archaea: +  
2: sp\_bacteria: +  
3: sp\_fungi: +  
4: sp\_human: +  
5: sp\_invertebrate: +  
6: sp\_mammal: +  
7: sp\_mhc: +  
8: sp\_organelle: +  
9: sp\_phase: +  
10: sp\_plant: +  
11: sp\_rodent: +  
12: sp\_virus: +  
13: sp\_vertebrate: +  
14: sp\_unclassified: +  
15: sp\_rvirus: +  
16: sp\_bacteriap: +  
17: sp\_archaeap: +

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	45	71.4	1053	16	Q9RK93
2	43	68.3	120	11	Q8C4A2
3	42	66.7	236	16	Q67934
4	42	66.7	595	4	Q727K2
5	41	65.1	97	12	Q99D18
6	41	65.1	279	17	Q8T0W3
7	40.5	64.3	1952	5	Q95SN5
8	40.5	64.3	4547	5	Q9W343
9	40	63.5	86	17	Q8TVM2
10	40	63.5	116	5	Q8VMN4
11	40	63.5	183	10	Q8RUL5
12	40	63.5	429	5	Q89538
13	40	63.5	1236	5	Q9NED7
14	39	61.9	196	2	Q89Q43
15	39	61.9	293	12	Q8QZ69
16	39	61.9	330	3	Q8WZT2
17	39	61.9	482	2	Q8VMJ2
18	39	61.9	548	11	Q80TQ4
19	38	61.9	637	16	Q7WKS9
20	39	61.9	637	16	Q7W8U9
21	39	61.9	2948	4	Q86WG6
22	38.5	61.1	1226	12	Q8JQ07
23	38.5	61.1	1226	12	Q8U206
24	38	60.3	101	17	Q8ZT29
25	38	60.3	157	11	Q8BLH8
26	38	60.3	185	11	Q8BKJ6
27	38	60.3	208	16	Q8ZML6
28	38	60.3	220	10	Q9LKA8
29	38	60.3	279	16	Q8YMW2
30	38	60.3	307	2	Q7X5S1
31	38	60.3	315	16	Q9KYU8
32	38	60.3	321	17	Q8ZU52
33	38	60.3	368	16	Q8LBA5
34	38	60.3	410	12	Q8BDP6
35	38	60.3	463	16	Q8G6A8
36	38	60.3	891	11	Q8B198
37	38	60.3	892	11	Q8B1B7
38	38	60.3	892	11	Q8B1E7
39	38	60.3	1035	5	Q2L380
40	38	60.3	1063	16	Q7U3R7
41	38	60.3	1187	5	Q8WR45
42	37.5	59.5	335	15	O41896
43	37.5	59.5	335	15	Q8ALT8
44	37	58.7	86	2	Q84CQ5
45	37	58.7	86	16	Q9K3I9

Q9RK93 streptomyce
Q8C4A2 mus musculus
Q67934 aquifex ae
Q727K2 homo sapien
Q99D18 bovine herp
Q8T0W3 methanopyru
Q95SN5 drosophila
Q9W343 drosophila
Q8TVM2 methanosarc
Q8VMN4 boltenia vi
Q8RUL5 oryza sativ
Q89538 caenorhabdi
Q9NED7 leishmania
Q8GQ43 pseudomonas
Q8QZ69 cucurbit le
Q8WZT2 neurospora
Q8VMJ2 pseudomonas
Q80TQ4 mus musculus
Q7WKS9 bordetella
Q7W8U9 bordetella
Q86WG6 homo sapien
Q8JQ07 rice black
Q8U206 rice black
Q8ZT29 pyrobaculum
Q8BLH8 mus musculus
Q8BKJ6 mus musculus
Q8ZML6 streptomyce
Q9LKA8 arabidopsis
Q8YMW2 anabaena sp
Q7X5S1 enterobacte
Q9KYU8 streptomyce
Q8ZU52 pyrobaculum
Q8LBA5 bacillus ce
Q8BDP6 rubus yello
Q8G6A8 bifidobacte
Q8B198 mus musculus
Q8B1B7 mus musculus
Q8B1E7 mus musculus
Q2L380 caenorhabdi
Q7U3R7 synechococc
Q8WR45 caenorhabdi
O41896 bovine foam
Q8ALT8 bovine foam
Q84CQ5 streptomyce
Q9K3I9 streptomyce

Search completed: May 19, 2004, 17:07:48  
Job time : 29.375 secs